Supplementary

Table S1 Details for primers sequences of real-time PCR

Genes	Forward Primer sequences	Reverse Primer sequences
МСМ3	GTCTACGGCAGGTATGACCA	GTAACGGTGCATCCGAAGGA
NLRC4	TCAGGACTTGAATGGACAAAGTCT	GTTGGTCCTTCCTCCACAGG
SPTBN1	ATGTGGACAAGGCCCTTCAG	TTGACATTGGGGTACCCAGC
ELP3	GGTGGATATCATTGCTGCCG	TCCACCAGGGCAGTATACACA
SLFN5	GAGTTTGTCATCTGCCACGC	CCACTCTGTCTGAAAATACTGGAA
RNASEL	GGACTTGGGAGAGCCGCTA	AGATCACCCACAGTGTTCTGG
GIMAP6	TGGAGCTGTCAGGAGGTCTA	CTGGGGCGGATAAGACGATG
GIMAP8	GATGCTGGCTCCTCCCTG	CTCCCGCTTGTTCTGGGTG
TRIM27	ATCAATGGTGCCATCACCCA	TGATTCTTTCAGCCCTGCTCA
SF3B3	TTGAGGTCTAATGGCGGACG	ACGGAGTCCAAGAAAGCCTG
HSPA8	TTGAACTCGCCTGCAGCTCT	CCCTTGGACATGGTTGCTGG
PIK3AP1	ATGGCAGCCTCAGGGGTG	AGGAACAGGGTCTGCAGGTA
RASSF2	ATGCCAAGCTCCACAGACTC	ACTAGGCGTCCTCACATTGC
PSEN1	ACCACCTGAGCAATACTAATGACA	CACATGCTTGGCGCCATATT
PPWD1	TTCGTAGTCACCTGGGAGTT	TTGCATCCCCTGGGCAATAG
COX6B1	GTGTCTTTGCTGAGGGTCAC	GCCATGGTGCTGAATCCTAAAG
POMP	GAGCTGCGGAAGATGAATGCC	AGCGGAGCAAATAGACCCTGA
FTL	GAGCCACTTCTTCCGCGAAT	TCATCTTCAGCTGGCTTCTTGA
EMP3	CAGCAGGGTGGGGCTTC	CAAAGTGGCCACGAAAAGCA
SF3B6	CGAACATTCGACTTCCACCTGA	TCTTCTGAAATGCCCTGTTGG
ATP5MD	GGGCCGAGAGGTGGTTACA	GGTGGGAACAAACAGCTGCC
POLR2L	GAGTACACCGAGGGGGATGC	TGAGCAGCTTCTCGATCAGG
HBE1	TTCCGACACAGCTGCAATCA	AAACAACGAGGAGTCTGCCC
β -actin	TTCCTTCCTGGGCATGGAGTC	TCTTCATTGTGCTGGGTGCC

Table S2 The sequences of siRNA used for TRIM27 and HMOX1 knockdown

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siRNA name	sequences	
siRNA negative control	5'-GUAUGACAACAGCCUCAAGTT-3'	
	5'-CUUGAGGCUGUUGUCAUACTT-3'	
TRIM27 siRNA-845	5'-GGAACAGGCACGAGCUGAATT-3'	
	5'-UUCAGCUCGUGCCUGUUCCTT-3'	
TRIM27 siRNA-1259	5'-GGAGAAAAUCCAAGAAUUATT-3'	
	5'-UAAUUCUUGGAUUUUCUCCTT-3'	
TRIM27 siRNA-1475	5'-GGUAGAGGUGGGAGAUAAATT-3'	
	5'-UUUAUCUCCCACCUCUACCTT-3'	
HMOX-1 siRNA	5'-CAGGCAAUGGCCUAAACUUCAdTdT-3'	

Table S3 Antibodies used in western blot

Antibody	Dilution	Cat No.	Manufacturer
TRIM27	0.736111111	12205-1-AP	Proteintech, Wuhan, China
HK-1/2	0.736111111	P07986	Promab, Changsha, China
PKM	0.736111111	10078-2-AP	Proteintech, Wuhan, China
LDHA	0.736111111	P06613	Promab, Changsha, China
GLUT1	0.736111111	P03992	Promab, Changsha, China
HMOX1	0.736111111	MAA584Hu22	Cloud-Clone Corp., Wuhan, China
β-Actin	1:40000	A3854	Sigma-Aldrich, Saint Louis, USA



Figure S1 GSEA revealed the highest enrichment is the glycolysis and gluconeogenesis KEGG pathway. GSEA was run with the TPMnormalized data and determined pathway-level ranking scores based on GSEA P values and NES. According to the ranking of the NES, the pathway with the highest enrichment score in the case group (malignant GGOs group) is the glycolysis and gluconeogenesis KEGG pathway. GSEA, Gene Set Enrichment Analysis; KEGG, Kyoto Encyclopedia of Genes and Genomes; NES, normalized enrichment score; GGO, ground-glass opacity; TPM, transcripts per kilobase million.



Figure S2 Verification of expression levels of the selected 23 DEGs in platelets samples. In 23 selected DEGs, 6 DEGs were no difference by HT-qPCR verification (P>0.01). Cancer: malignant GGOs, in red; Inflammation: benign GGOs, in green. The left vertical axis represents average $2^{-\Delta\Delta Ct}$ (relative to the internal reference β -actin) using to evaluate mRNA levels, cancer =56; inflammation =66. DEGs, differentially expressed genes; HT-qPCR, high-throughput quantitative polymerase chain reaction; GGO, ground-glass opacity.



Figure S3 The protein expression of glycolysis factor in tissues. Western blot was used to measure the protein expression of HK1/2, PKM1/2, LDHA and GLUT1 in the seven paired NSCLC and adjacent tissues (upper). The densities of each band were quantified by the Image J program (lower). **, P<0.01; ***, P<0.001 *vs*. β-actin.



Figure S4 The protein expression of TRIM27 and HMOX1 in tissues. Western blot was used to detect the protein expression of TRIM27 and HMOX1 in the seven paired NSCLC and adjacent tissues (upper). The densities of each band were quantified by the Image J program (lower). ***, P<0.001 $vs. \beta$ -actin.